

Rev. *Florilegium* 2013

WO 2005/037989

PCT/US2003/024918

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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<210> 357

<211> 1536

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<213> Artificial Sequence

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<223> fusion polynucleotide

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<211> 1696

<212> □

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<220>

<223> fusion polynucleotide

<400> 358

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<210> 359

<211> 141

<212> PRT

<213> Artificial Sequence

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<223> fusion polypeptide

<400> 359

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Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu	35	40	45	
Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu	50	55	60	
Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala	65	70	75	80
Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln	85	90	95	
Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr	100	105	110	
Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Ala Met	115	120	125	
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser	130	135	140	

<210> 360

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 360

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Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu	35	40	45	
Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile	50	55	60	
Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln Val Phe Phe	65	70	75	80
Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala	85	90	95	
Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Ala Met Asp Tyr Trp	100	105	110	
Gly Gln Gly Thr Ser Val Thr Val Ser Ser				

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115
120

<210> 361
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 361
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20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

<210> 362
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 362
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Ser Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
210 215 220
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
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Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
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Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
260 265 270

<210> 363
<211> 505
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 363
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
210 215 220
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
225 230 235 240
Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
245 250 255
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
260 265 270
Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
275 280 285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
290 295 300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305 310 315 320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys 500 505

<210> 364

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 364

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 20 20 25 30
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 35 40 45
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 50 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 85 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 100 105 110
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 115 120 125
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
 130 130 135 140
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
 145 145 150 155 160
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 165 165 170 175
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
 180 180 185 190
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
 195 195 200 205
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr
 245 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
 275 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 325 330 335

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
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Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
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Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
515 520 525
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
530 535 540
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
545 550 555

<210> 365

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y

<400> 365

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gtagaaggag cc 72

<210> 366

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A

<400> 366

gttgttgaag acgttccct gctgccacct gctcttgccc acggtagct tgctgttagag 60
ggcgaaggag cc 72

<210> 367

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' oligo to introduce mutation in CH3 at position
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<400> 367

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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gaagaaggag cc 72

<210> 368
<211> 72
<212> DNA
<213> Artificial Sequence

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<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y and 407 to A

<400> 368
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gtagaaggag cc 72

<210> 369
<211> 72
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<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A and 407 to Y

<400> 369
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<210> 370
<211> 324
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<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tgggagagca atgggcagcc ggagaacaac tacaagacca cgccctccgt gctgtaccc 180
aacggctct tctaccccta tagcaagctc accgtggaca agagcagggt gcagcagggg 240
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<220>
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<400> 371
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgccctccgt gctgtaccc 180
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cttccctgt ccccggttaa atga 324

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WO 2005/037989

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<223> fusion polynucleotide

<400> 372

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 373

<211> 324

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<223> fusion polynucleotide

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 374

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<223> fusion polynucleotide

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tggagagaca atgggcagcc ggagaacaaac tacaagacca cgcccccgt gctggactcc 180
gacggctctc tcttcctcgc cagaacgctc accgtggaca agagcaggta gcacggggg 240
aacgtttctc catgtcccgat gatgcattgg gctctgcaca accactacac gcagaagagc 300
cttcgggtaa atgaa 324
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<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 375

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								20			25		30		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
				35			40			45					
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
				50			55			60					
Tyr	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
				65			70			75			80		
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85				90				95			

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 376
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 376
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 377
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 377
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Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 378
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
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<400> 378
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

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49076.000004pct2 10.207,655 Seq List Text 07.24.03.txt
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
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 85 90 95
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 100 105

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<220>
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<400> 379
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1 5 10 15
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 380
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
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 ccaggggaga aggcttgcagg gacttgcagg gccaggctca gtgtaaagttt catgtactgg 120
 taccggcaga aqccaggatc cttccccaat ccctggattt atggcccatc caaacctggct 180
 tctggagttc ctgtctcgctt ctagggcagg gggctcgaaa cctcttactt tcttcacaatc 240
 aqgacgttgg aqgcttgcaga tgctgcact tattatcgcc aqgactggag tttaaccca 300
 cccacgttcg gtgtctggac caaggctggat ctggaaatggat gggctggcttc gggcgtgtt 360
 ggatctggaa gaggctggggat ctctcaggat tattatcgcc aqgactggag tttaaccca 420
 aggcttgggg ccttcaggaa gtgtctggat aqgactggat gggctggcttc gggcgtgtt 480
 aatatgcact ggatctggaa ctatgtctgg aqgactggat gggctggcttc gggcgtgtt 540
 ccaggaaatg ggtatcttc ctacaatcg aqgacttgcgg gcaaggccac actgactgtt 600
 gacaatctt ccaggcagac ctatcatgcg ctccggccgg tggatctgg aqgactggat 660
 gtcttattttt gtgtcaaggat ggttgcactt aqgacttgcgg tggatctgg aqgactggat 720
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 gtgtcataatg ccaagaaaaa ggcggcgggat gggatcttc aqgacttgcgg tggatctgg 1020
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 agcgttctca cccgttccatcccccggccccc gggatcttc aqgacttgcgg tggatctgg 1140

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<210> 381

<211> 1521

<212>

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<220>

<223> fusion polynucleotide

<400> 381

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ccaggggaga	aggtcacaat	gacttgcagg	ggccatgtca	catgcattgg	180	
tatccaggca	aggccaggat	ttcccccaaa	ccctttgttt	atgcggccat	240	
ttggtagtcc	ctctgcqctt	caatgtggcgt	gggtttttggaa	ccatgtttttcc	300	
acaggatgg	aggcttggaa	tgcgtccggat	ttatataccgt	tttttttttttt	360	
cccaatgttc	gtgtttgggg	catctttttttt	tttttttttttt	ggggccgttt	420	
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aatggggcage	ccatggggaa	tttttttttttt	tttttttttttt	tttttttttttt	1320	
tttttacccat	tttttacccat	tttttttttttt	tttttttttttt	tttttttttttt	1380	
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<210> 382

<211> 1515

212

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 382

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 aatgggcagc cggagaacaa ctacaaggcc acggctcccg tgctggactc cgacggctcc 1380
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<210> 383

<211> 1515

<212> DNA

<213> Artificial Sequence

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 ccaggggggaa aggttcaat gacttgcggg gccaggctcaa gtgtaaatgtt cttgtactgg 180
 taccatggcc agccggatgc cttcccaaa ccctgtggatcc atggccctatc caactgttcc 240
 tctgggttcc ctgtctgttcc cttgtggactt cttgtgggggg cttcttactt tcttcataatc 300
 agcagatggc aggttcaatgg tgcgttccat tattatgtcc agcgtgtgggg ttttaacca 360
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 aggcttgggg ccgttgcggaa gatgttccgttcc cttgttccgttcc gtttccatgtcc taccatgttcc 540
 aatatgtccat ggtttaatggc gacccatgttcc cttgttccgttcc gtttccatgtcc taccatgttcc 600
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 gacaaaatcc ccacggccatcc ctatgttcc cttgttccgttcc gtttccatgtcc taccatgttcc 720
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 ggcacacggg cccaggccatcc ctgttccgttcc gtttccatgtcc taccatgttcc taccatgttcc 840
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 ttccttcctg ccacggactt caccgtggac aagagcagggt ggcggcagggg gaacgtcttc 1440
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<210> 384

<211> 1515

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 384

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 ccaggggggaa aggttcaat gacttgcggg gccaggctcaa gtgtaaatgtt cttgtactgg 180
 taccatggcc agccggatgc cttcccaaa ccctgtggatcc atggccctatc caactgttcc 240
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ggatctgggg	gggggtgggg	ttttccgggt	tatccacgt	ggggcggtgt	420
aggctgggg	ttttccgggt	ttttccgggt	tatccacgt	tgaggctgggg	480
aatatcggt	ttttccgggt	ttttccgggt	ttttccgggt	ttttccgggt	540
cccgaaatgt	ttttccgggt	ttttccgggt	ttttccgggt	ttttccgggt	600
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<210> 385
<211> 500

<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 385	Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser	
35 40 45	
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser	
50 55 60	
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro	
65 70 75 80	
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile	
85 90 95	
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp	
100 105 110	
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys	
115 120 125	
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser	
130 135 140	
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala	
145 150 155 160	
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	
165 170 175	
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile	
180 185 190	
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe	
195 200 205	
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr	
210 215 220	
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	
225 230 235 240	
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp	
245 250 255	
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser	
260 265 270	
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu	
275 280 285	

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 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Glu Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
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 485 490 495
 Ser Pro Gly Lys 500

<210> 386

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220

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 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
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<210> 387

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> fusion polypeptide

<400> 387

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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

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 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Gly Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Val Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
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<210> 388

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 388

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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

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 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser ser ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
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 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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 Ser Pro Gly Lys
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<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 389

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asp Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
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 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
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 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
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 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
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 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
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 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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 485 490 495
 Ser Pro Gly Lys 500

<210> 390

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> 5' oligo to mutat IgG1

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 <210> 391
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 <223> 5' oligo to mutate IgG1

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 <210> 392
 <211> 63
 <212> DNA
 <213> Artificial sequence
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 <223> 5' oligo to mutate IgG1

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 <210> 393
 <211> 1521
 <212> DNA
 <213> Artificial sequence
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 <223> fusion polynucleotide

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 ccaggggaga aaggctcaat gacttgtcgg gccaggatctaa gtgtaaaggta catgcacttg 180
 taccggcaga agccaggatc tcccccccaat ccttggattt atgccccatc caacctggct 240
 ttctggagtc ctgttcgttctt cttggcggatgg ggttgcgggaa ccctttttttt tccatcaatc 300
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 cccatcggtt ctgttcgttctt ccaggatggatgg ctgttttttttccatcaatc 420
 ggatctgggg aagggttttttccatcaatc 480
 agggcttgggg ctttcgttctt ccaggatggatgg ctgttttttttccatcaatc 540
 aatatgcactt ggttttttttccatcaatc 600
 ccaggaaatgg gtgtatatttttccatcaatc aaggatggatgg aatggatgg agttttttttt 660
 gacaaaatcc tccatcaatc aaggatggatgg aatggatgg agtttttttttccatcaatc 720
 gtcttatttttccatcaatc 780
 gtgtcaaggatgg ttttttttttccatcaatc 840
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 gtggcatatgg gtttttttttccatcaatc 1020
 gtttttttttccatcaatc 1080
 agccgttcttc tccatcaatc 1140
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 cgaggaaatcc tccatcaatc 1260
 aggttgcatttccatcaatc 1320
 agccgttcttc tccatcaatc 1380
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 tcatgttcgg ttttttttttccatcaatc 1560

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<210> 395
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<213> Artificial Sequence

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<223> fusion polypeptide

<400> 396

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Ser Ser Val Ser Tyr Met His Trp Tyr Gln Lys Pro Gly Ser Ser
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Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65          70          75          80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85          90          95
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100          105          110
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130          135          140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145          150          155          160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165          170          175
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195          200          205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
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275          280          285
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Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
370          375          380
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440 445
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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485 490 495
Ser Pro Gly Lys 500

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<212> PRT
<213> Artificial sequence

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Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Ser Ser
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Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
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245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
260 265 270
Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu
275 280 285
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
290 295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

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 340 345 350
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 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 398

<211> 500

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 398

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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
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 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Ser Ser Asp Gln Glu Pro Lys Ser

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 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Glu Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
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 Ser Pro Gly Lys
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 atgaccctgtaa agaccaggtaa gaataattggc acaatcttaa actggatatac cccaaaaccca 180
 aaggaggctc caagggtctt catcaatgtt gcttcgcagtt cccattccgg gatccccctcc 240
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 gatgatatacg gaaatttatca ctgtcaacatc agtagaaatgtt ggccgtgtcac gtcccggtct 360
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 aaaaacaaatc ctggggaaatgg attagggaaatgtt ttatgggtgg aatgtgggt 600
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 acacgttaca tggaaactcgac cagcttgacaa tctggaggat ctgtccatcta ttactgtgca 720
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 Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
 35 40 45
 Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
 50 55 60
 Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
 85 90 95
 Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
 100 105 110
 Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
 130 135 140
 Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
 145 150 155 160
 Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
 165 170 175
 Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
 180 185 190
 Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
 195 200 205
 Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
 210 215 220
 Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
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<213> Artificial sequence

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<223> oligonucleotide primer

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<211> 47

<212> DNA

<213> Artificial sequence

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<213> Artificial Sequence
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<223> oligonucleotide primer

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<211> 48
<212> DNA
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cgcggtcaga gccggcttaga cttcttcctt atgcgtctgg agcagaacgc cttggagccc 180
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cgcgttcaaaat ttcagacac caagatgcac agcgttcggc acagataaccc cccgcacccgt 420
acgttgcgtt tgccggagtc actgagaacaa cagagaaggaa gaacgcacaa 480
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caaggatgttcc acgaggccccg tgaccctccat aacaggatgtt gggccatgttc cccgtatgtc 600
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<211> 211
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20 25 30
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
35 40 45
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
50 55 60
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65 70 75 80
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly
85 90 95
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
100 105 110
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
115 120 125
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
130 135 140
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
145 150 155 160
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
165 170 175
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
180 185 190
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
195 200 205
Glu Ala Ser
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 ctggagcgcg tgcagagttt cttggacactt ttacacgttc tgcttgagaca gaacgacactt 180
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<223> fusion polypeptide

<400> 418

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 Ser Gly Ser Leu Ser Gly Asn Asp Leu Met Glu Leu Lys Phe Leu Cys
 20 25 30
 Arg Glu Arg Val Ser Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu
 35 40 45
 Asp Leu Phe Thr Val Leu Leu Glu Gln Asn Asp Leu Glu Arg Gly His
 50 55 60
 Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu
 65 70 75 80
 Leu Gln Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro
 85 90 95
 Pro Gly Glu Ala Asp Leu Gln Val Ala Phe Asp Ile Val Cys Asp Asn
 100 105 110
 Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu
 115 120 125
 Ala Lys Met Asp Gly Ile Glu Lys Tyr Pro Arg Ser Leu Ser Glu
 130 135 140
 Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn
 145 150 155 160
 Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn
 165 170 175
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 Glu Asn Met Ser Pro Val Leu Arg Asp Ser Thr Val Ser Ser Ser Glu
 195 200 205
 Thr Pro
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48

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<212> DNA
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<400> 426
gttgttatacg atgcatgctc aatcagaagg gaagacaagt tttttct 48

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